

FIGURE 1

1 ATG GCG GAT ACA GCT AGA GGA ACC CA? CAC GAT ATC ATC GGC AGA GAC CAG TAC CCG ATG 60
1 M A D T A R G T H H D I I G R D Q Y P M 20

61 ATG GGC CGA GAC CGA GAC CAG TACCAG ATG TCC GGA CGA GGA TCT GAC TAC TCC AAG TCT120
21 M G R D R D Q Y Q M S G R G S D Y S K S 40

121 AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT GTT CTC TCC 180
41 R Q I A K A A T A V T A G G S L L V L S 60

181 AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC GTT ATC 240
61 S L T L V G T V I A L TV A T P L L V I 80

241 TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGTTTT CTT300
81 F S P I L V P A L I T VA L L I T G F L 100

301 TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AAG TAC GCA 360
101 S S GGF G I A A I TVF SW I YKYA 120

361 ACG GGA GAG CAC CCA CAG GGATCA GAC AAG TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC 420
121 T G E H P Q G S D K L D S A R M K L G S 140

421 AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA 430
141 K A Q D L K D R A Q Y Y G Q Q H T G G E 160

481 CAT GAC CGT GAC CGT ACT CGT GGTGGC CAG CAC ACT ACT TAA
161 H D R D R T R G G Q H 1 T *

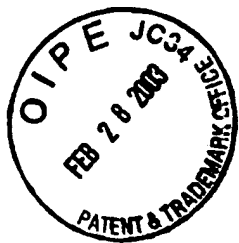
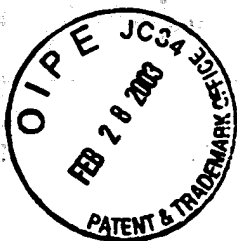


FIGURE 2A

1 ctatacccaacctcggg~ttgg~cacaccaggaactctctggttaagctagctccactccccagaaacaaccggcgccaaa 80
81 ttgccggaattgctgacctgaagacggaacatcatcgctcggtccttggggcattgcggcggaagatgggtcagcttggg 160
161 cttgaggacgagaccgaatcgagctctgttgaaaggtgttcattgggatttgtatacggagattggctcgtcagagaggtt 240
241 tgagggaaaggacaaatgggttggctctgggaaagagagtgcggttttagagagagaattgagaggttttagagagaga 320
321 tgcggcgcgatgacggggaggagagacgacgagga~ctgcattatcaaagcagtgacgtggtgaaatttgaacttttaa 400
401 gaggcagatagattttattatttgtatccattttcttcattgttctagaatgtcgggaacaaattttaaaactaaat~~t 480
481 aaatttttctaattttgttgccaatagtgatgtgtggccgtatagaaggaatctattgaaggcccaaacccatactga 560
561 cgagcccaaagggttcgttttgcgttttatgtttcggttcgatgccacgccacattctgagctaggcaaaaaacaaa~~gt 640
641 gtctttgaatagactcctctcgttaacacatgcagcggtgcatggtgacgccattaacacgtggcctacaattgcatga 720
721 tgtctccattgacacgtgacttctcgtctcctttcttaatatctaaacacactcctacctcttccaaaatatataca 800
801 catctttttgatcaatctctcattcaaaatctcattctctctagtaacaagaacaaaaaa ATG GCG GAT ACA 873
1 M A D T 4
874 GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC 933
5 A R G T H H D I I G R D Q Y P M M G R D 2 4
934 CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT 993
25 R D Q Y Q M S G R G S D Y S K S R Q I A 4 4
994 AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CT? ACCCTT 1053
45K A A T A V T A G G S L L V L S S L T L 64
1054 GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC 1113
65 V G T V I A L T V A T P L L V I F S P I 84
1114 CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG 1173
85L V P A L I T V A L L I T G F L S S G G 104
1174 TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatcttact 1239
105 F G I A A I TVF S W I YK 118
1240 tcataattttgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgta 1319
1320 acaataagaaattgcaaattctagggaaacatttgggttaactaaatacgaatttgacctagctagcttgaatgtgtctgt 1399
1400 gtatatcatctatataggtaaaatgcttgggtatgata~ctattgattgtgaatag G TAC GCA ACG GGA GAG 1470
119 Y A T G E 123



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FIGURE 2B

1471 CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG 1530
124 H P Q G S D K L D S A R M K L G S K A Q 143

1531 GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT GGT TGG GAA CAT GAC 'XT 1590
144 D L K DRAQ Y Y G Q Q H T GWE H D R 163

1591 GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT GCG ATC GAA GGG AGA ATC ACT TAC ACT GAC 1650
164 D R T R G G Q H T T A I EGR I T Y T D 183

1651 TGT ACT GAA TCT GGA CAG AAC CTC TGT CTC TGT GAA GGA TCT AAC GTT TGT GGA AAG GGA 1710
184 C T E S G Q N L C L c E G S N V C G K G 203

1711 AAC AAG TGT ATC CTC GGA TCT AAC GGA AAG GGA AAC CAG TGT GTT ACT GGA GAA GGA ACT 1770
204 N K C I L G S N G K G N Q C V T G E G T 223

1771 CCA AAC CCA GAA TCT CAC AAC AAC GGA GAC TTC GAA GAA ATC CCT GAA GAA TAC CTC CAG 1830
2 2 4 P N P E S H N N G D F E E I P E E Y L Q 243

1831 TAA gtcgactctagacggatctcccgatcggttcaaacatttggcaataaaagtttcttaagattgaatcctgttgccggt 1909
244 * 244

1910 cttgcgatgattatcatataatttctgttgaattacgttaagcatgtaataattaacatgtaatg-atgacgttat-tat 1989

1990 gagatgggtttttatgattagagtcgcaattatatacatttaatacgcgatagaaaacaaaatatagcgcgcaaaactagg 2069

2070 ataaattatcgcgcggtgtcctatgttactagatcGGAATTC 2115

The diagram illustrates the construction of the pCGBHIRT plasmid through a series of cloning steps:

- pUCOBILT (4598 bp)** and **pHir (2916 bp)** are the starting plasmids.
- pUCOBILT contains: Ap, ORI, lacI, lacZ, NOS, and OBIL.
- pHir contains: Ap, lacZ, lacI, ORI, and Hirudin.
- pUCOBILT is cut with **PstI** and **PvuI**.
- pHir is cut with **PvuI** and **Sall**.
- The fragments are ligated into pUCOBILT to form **pUCOBHIRT (4797 bp)**.
- pUCOBHIRT contains: Ap, ORI, lacI, lacZ, NOS, Hirudin, and oleosin.
- pUCOBHIRT is cut with **HindIII** and **EcoRI**.
- The fragments are ligated into **pBluescript+** to form **pBIOBHIRT (5075 bp)**.
- pBIOBHIRT contains: Ap, ORI, lacI, lacZ, NOS, Hirudin, and oleosin.
- pBIOBHIRT is cut with **PstI** and **HindIII**.
- The fragments are ligated into **pCGN1559** to form the final **pCGBHIRT (16515 bp)**.
- pCGBHIRT contains: ori ColEI, Gm, ori pRI, LB, 3'tml-npt-35S, and oleosin.

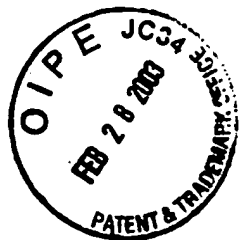
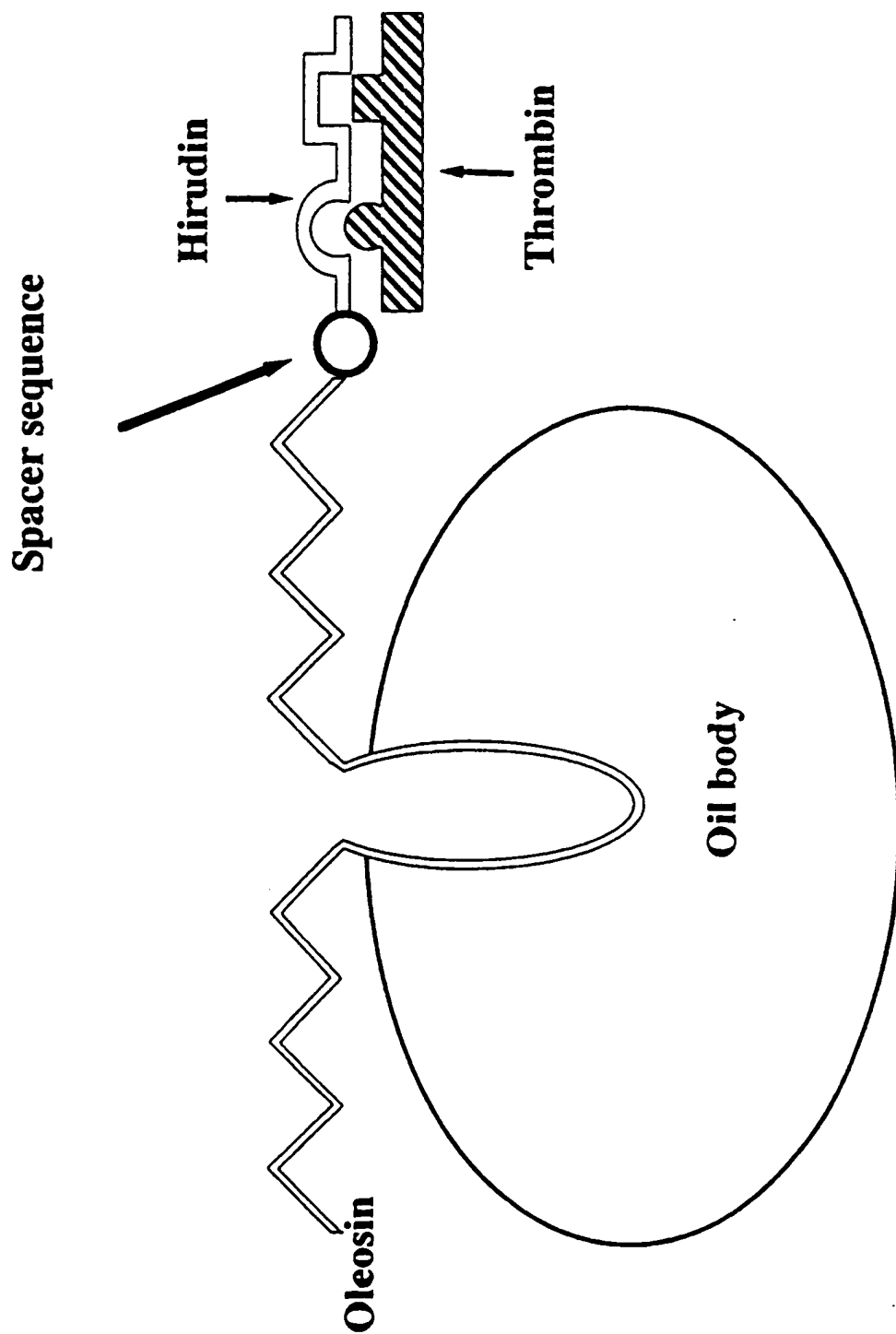


FIGURE 4



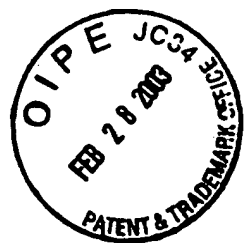


FIGURE 5

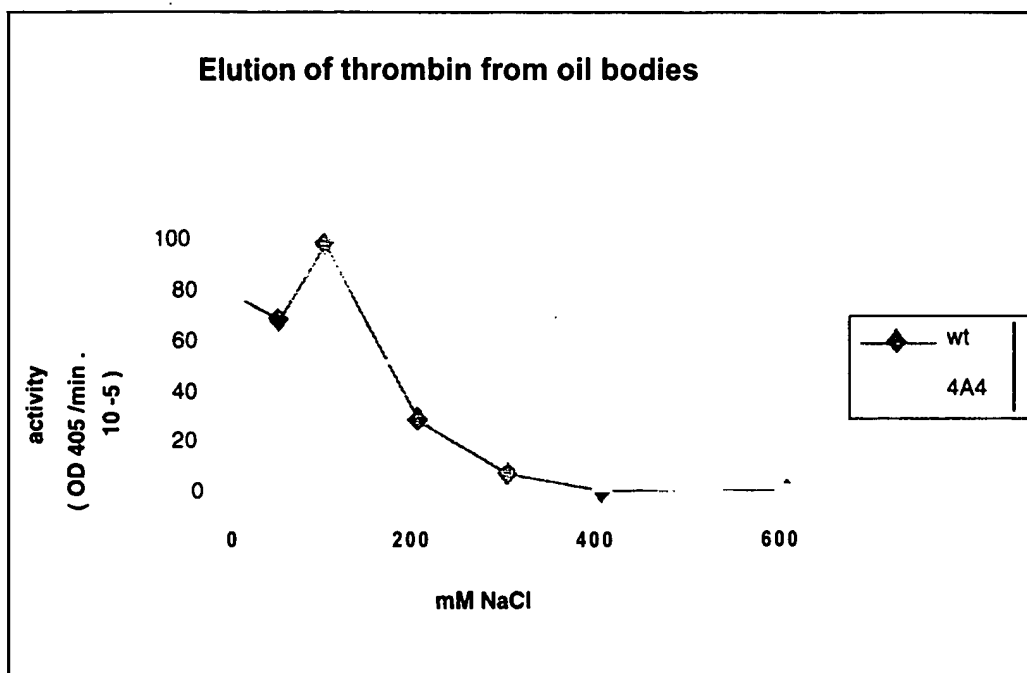
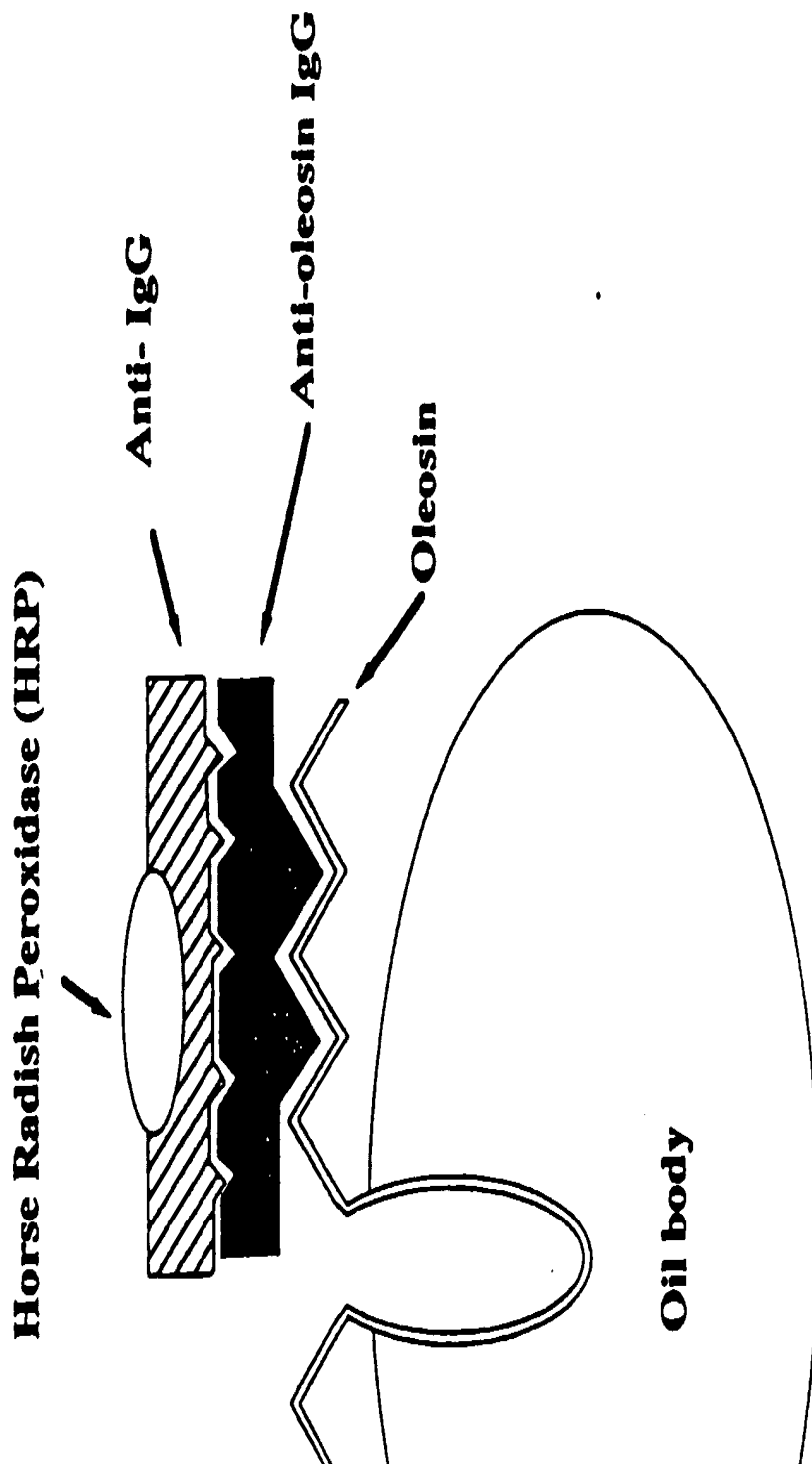




FIGURE 6



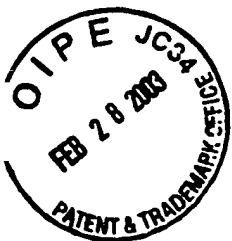
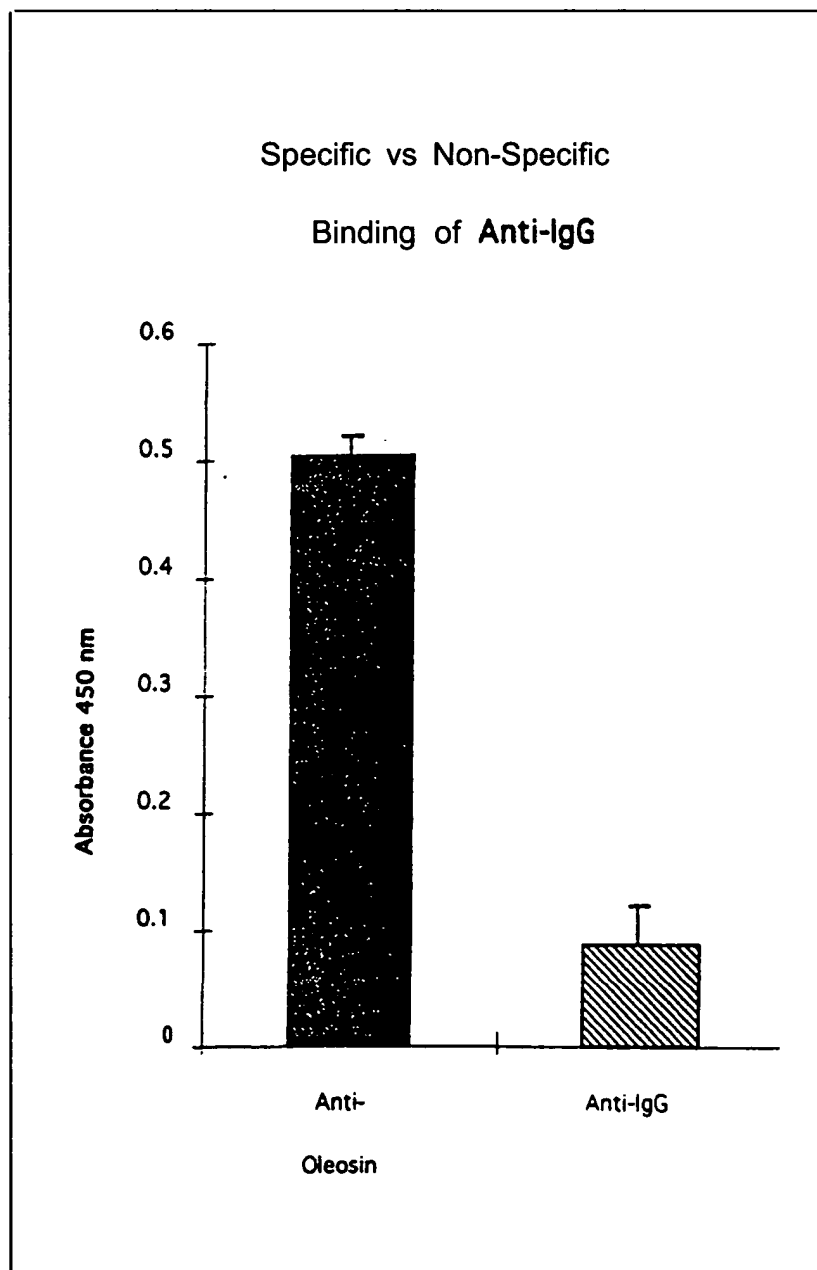


FIGURE 7



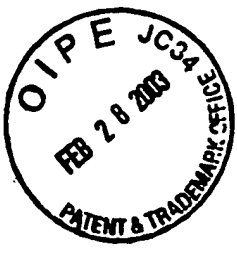


FIGURE 8A

1 gagctcaaatacgaatctgataactgataacgtctagatcttttaggggttaaagcaatcaatcacctgacgattcaaggtggt 80
81 tggatcatgacgattccagaaaacatcaagcaagctctcaagctacactctttgggatcatactgaactctaacaacct 160
161 cgttatgtcccgtagtgccagtagacacatcctcgtaactcggattatgcacgatgccatggctatacccaacctcggtc 240
241 ttgggtcacaccaggaactctctggttaagctagctccactccccagaaaacacggcgccaaattgccggaattgctgacc 320
321 tgaagacggaacatcatcgctcgggt-cttggggcgattgcggcggaagatgggtcagcttgggcttgaggacgagacc-ga 400
401 atcgagctctgttgaaggttgttcattgggatttgtatcaggagattggctcgcgagaggtttgagggaaaggacaaatg 480
481 ggtttggctctgggaaaagagagtg-gggcttttagagagagaattgagaggttttagagagagatgcggcgcgatgacggg 560
561 aggagagacgacgaggacctgcattatcaagcagtgacgtggtaaatgtggaacttttaagaggcagatagatttatt 640
641 atttgtatccattttcttcattgtt-tagaatgtcgcggaacaaattttaaaactaaatcctaaatttttctaattttgt 720
721 tgccaatagtggatgtggtg-cgtatagaaggaat-tattgaaggcccaaacccatactgacgagcccaagggttcgtt 800
801 ttgcgttttatgtttcggttcgtatg-caacg-cacattctgagctaggcaaaaaacacgtgtctttgaaatagactcct 880
881 ctcgttaacacatgcagcggctgcatggtgacgccattaacacgtggcctacaattgcatgatgtctccattgacacgtg 960
961 acttctcgtctccttttcttaatatatacacaacactcctacctcttccaaaatatatacacatctttttgatcaatct 1040
1041 ctcattcaaaatctcatrctctctagtaaacaggatccccctcgcggcgccg ATG GCG GAT ACA GCT AGA ACC 1112
1 M A D T A R T 7
1113 CAT CAC GAT GTC ACA AGT CGA GAT CAG TAT CCC CGA GAC CGA GAC CAG TAT TCT ATG ATC 1172
8 H H D V T S R D Q Y P R D R D Q Y S M I 27
1173 GGT CGA GAC CGT GAC CAG TAC TCT ATG ATG GGC CGA GAC CGA GAC CAG TAC AAC ATG TAT 1232
28 G R D R D Q Y S M M G R D R D Q Y N M Y 47
1233 GGT CGA GAC TAC TCC AAG TCT AGA CAG ATT GCT AAG GCT GTT ACC GCA GTC ACG GCG GGT 1292
48 G R D Y S K S R Q I A K A V T A V T A G 67
1293 GGG TCC CTC CTT GTC CTC TCC AGT CTC ACC CTT GTT GGT ACT GTC ATT GCT TTG ACT GTT 1352
68 G S L L V L S S L T L V G T V I A L T V 87
1353 GCC ACT CCA CTC CTC GTT ATC TTT AGC CCA ATC CTC GTG CCG GCT CTC ATC ACC GTA GCA 1412
88A T P L L V I F S P I L V P A L I T V A 107
1413 CTT CTC ATC ACT GGC TTT CTC TCC TCT GGT GGG TTT GCC ATT GCA GCT ATA ACC GTC TTC 1472
108 L L I TG F L S SGGFAIAA I TVF 127
1473 TCC TGG ATC TAT AAG TAC ACA ACG GGA GAG CAC CCA CAG GGG TCA GAT AAG TTG GAC AGT 1532
128 S W I Y K Y A T G E H P Q G S D K L D S 147
1533 GCA AGG ATG AAG CTG GGA ACC AAA GCT CAG GAT ATT AAA GAC AGA GCT CAA TAC TAC GGA 1592
148 A RMK L G T KAQ D I KDRAQ YYG 167
1593 CAG CAA CAT ACA GGT GGT GAG CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT 1652
168 Q Q H T G G E H D R D R T R G G Q H T T 187
1653 CTC GTT CCA CGA GGA TCC ATG GAT CCC AAC TGC TCC TGT GCC GCC AGT GAC TCC TGC ACC 1712
188 L V P RG S M D PNC S CAA S D SC T 207

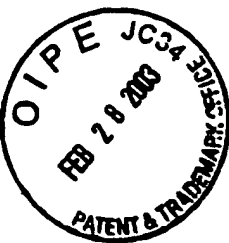


FIGURE 8B

1713 TGC GCC GGC TCC TGC AAG TGC AAA GAG TGC AAA TGC ACC TCC TGC AAG AAA AGC TGC TGC 1772
208 C A G S C K C K E C K C T S C K K S C C 227

1773 TCC TGC TGT CCT GTG GGC TGT GCC AAG TGT GCC CAG GGC TGC ATC TGC AAA GGG GCG TCG 1832
228 S C C P V G C A K C A Q G C I C K G A S 247

1833 GAC AAG TGC AGC TGC TGT GCC TGA gcggccgcgagggtgcagaatgagttccaagatggtttgtgacgaag 1904
248 D K C S C C A , 255

1905 ttagttgggtgtttttatggaactttgtttaagcttgtaatgtggaagaacgtgtggctttgtggtttttaaatggttg 1984

1985 tgaataaagatgtttcctttggattaactagtatttttctattggtttcatggttttagcacacaacattttaaatatg 2064

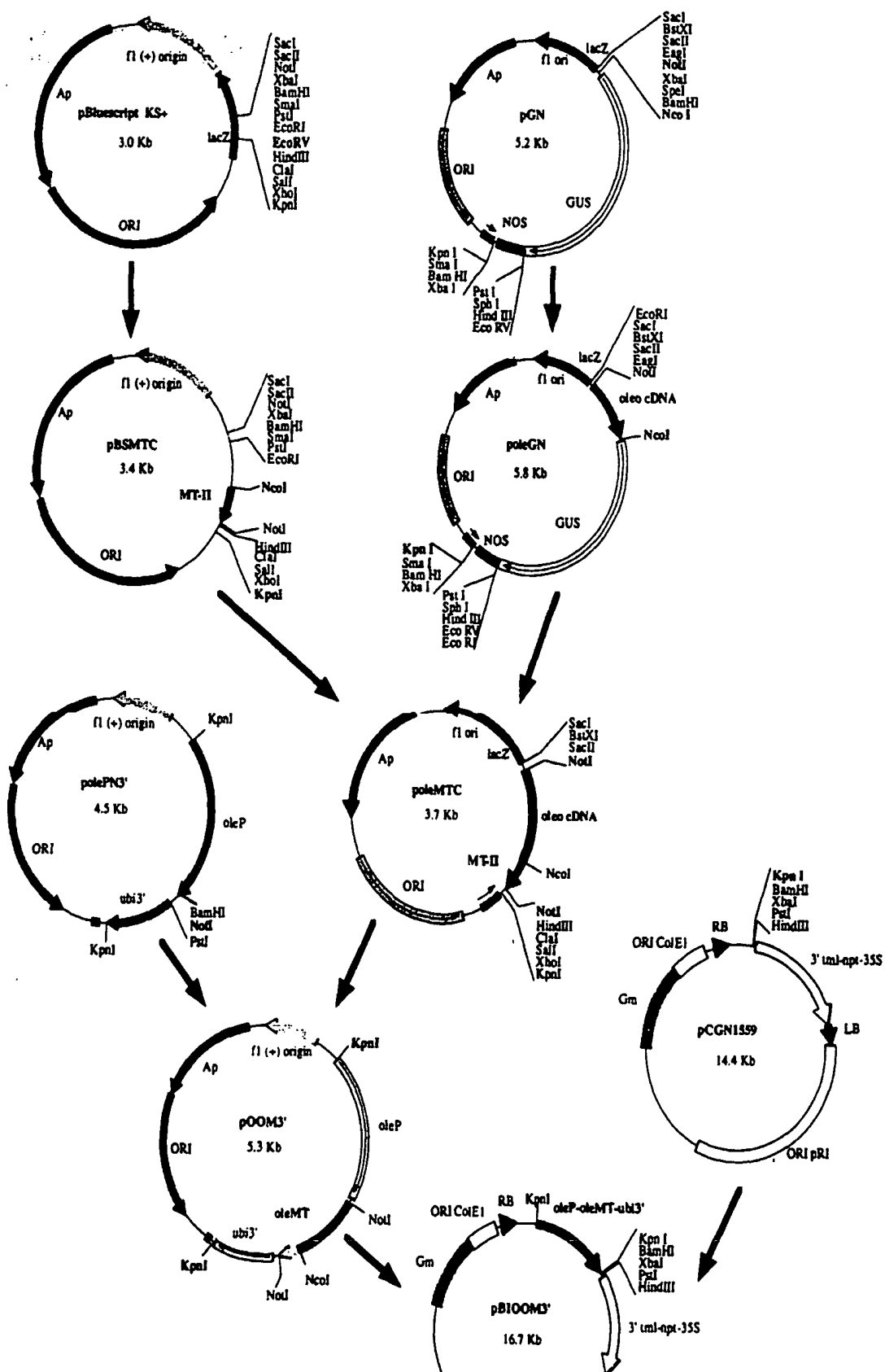
2065 ctgtagatgatatgctgcctgctttattatttacttaccctcaccttcagtttcaaagttgttgcaatgactctgtgt 2144

2145 agtttaagatcgagtgaagtagattttgtct atatttattaggggtatttgatgctaataaggtaaacatgggtttatga 2224

2225 cagcgtacttttttggttatggtgttgacgtttccttttaacattatagtagcgtccttggtctgtgttcattggttga 2304

2305 acaaaggcacactca~ttggagatgcggtctccactgatatttgaacaaagaattcggtacc 2366

FIGURE 9



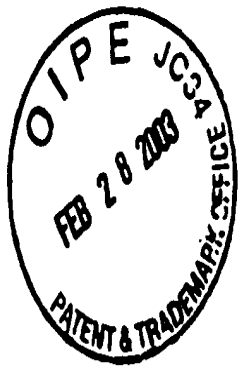
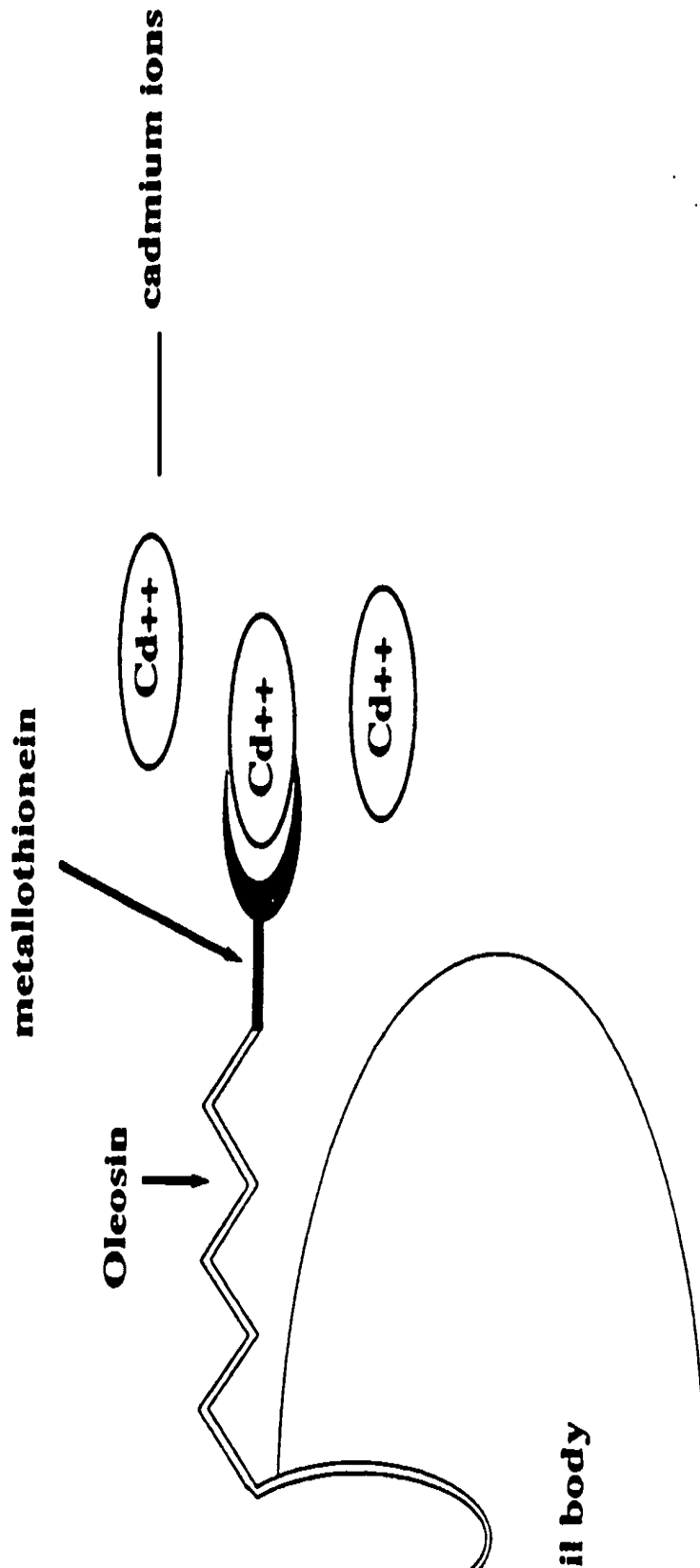


FIGURE 10



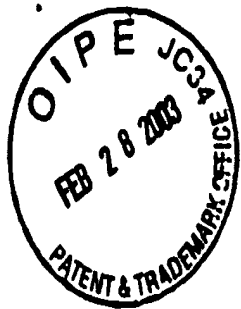
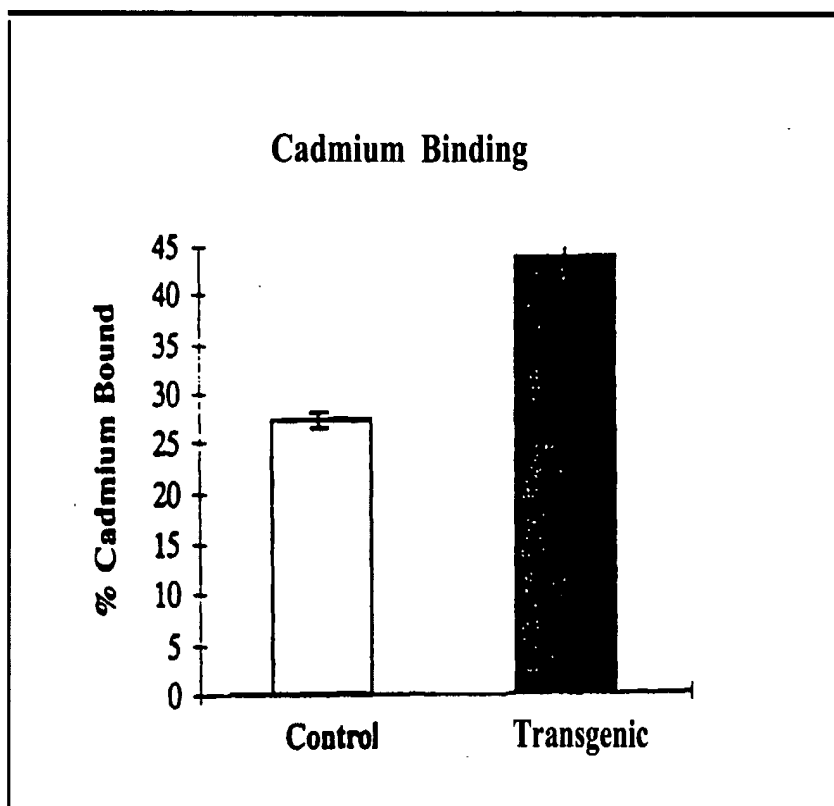


FIGURE 11

A



B

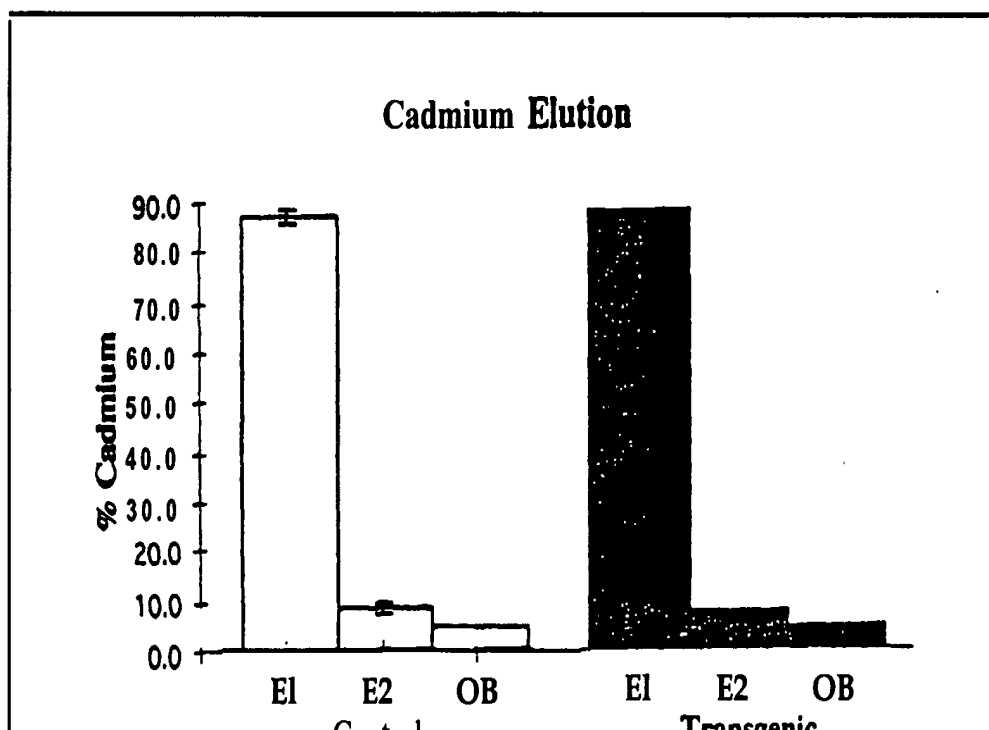
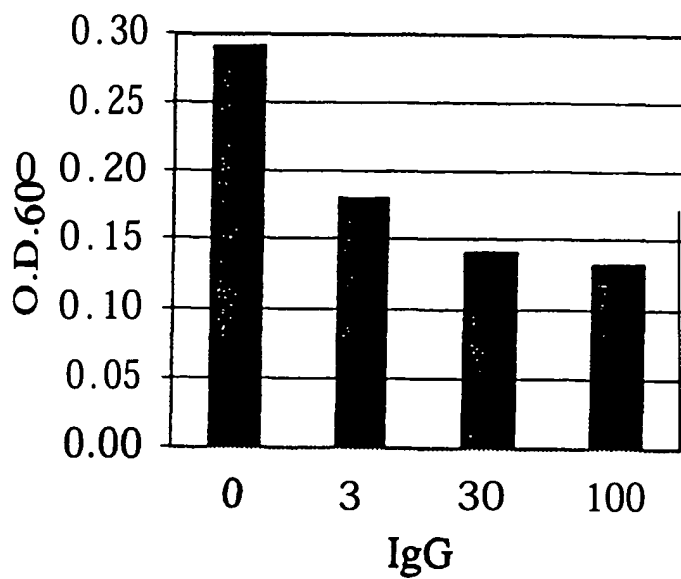
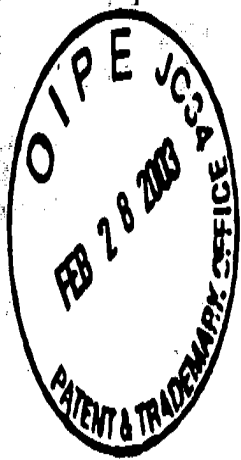




FIGURE 12





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FIGURE 13

NcoI

1 CTCC ATGGATCAACGCAATGGTTTT ATC CAA AGC CTT AAA GAT GAT CCA AGC CAA AGT GCT 61
1 M D Q R N G F I Q S L K D D P S Q S A 19

62 AAC GTT TTA GGT GAA GCT CAA AAA CTT AAT GAC TCT CAA GCT CCA AAA GCT GAT GCG CAA 121
2 O N V L G E A Q K L N D S Q A P K A D A Q 3 9

122 CAA AAT AAC TTC AAC AAA GAT CAA CAA AGC GCC TTC TAT GAA ATC TTG AAC ATG CCT AAC 181
40 Q N N F N K D Q Q S A F Y E I L N M P N 59

182 TTA AAC GAA GCG CAA CGT AAC GGC TTC ATT CAAAGT CTT AAA GAC GAC CCAAGC CAAAGC 241
60 L N E A Q R N G F I Q S L K D D P S Q S 7 9

242 ACT AAC GTT TTA GGT GAA GCT AAA AAA TTA AAC GAA TCT CAA GCA CCG AAA GCT GAT AAC 301
80 T N V L G E A K K L N E S Q A P K A D N 9 9

302 AAT TTC AAC AAAGAACAACAAAT GCT TTC TATGAAATC TTG AAT ATG CCT AAC TTA AAC 361
100 N F N K E Q Q N A F Y E I L N M P N L N 119

362 GAA GAA CAA CCA AAT GGT TTC ATC CAA AGC TTA AAA GAT GAC CCA AGC CAA AGT GCT AAC 421
120 E E Q R N G F I Q S L K D D ? S Q S A N 139

422 CTA TTG TCA GAA GCT AAA AAG TTA AAT GAA TCT CAA GCA CCG AAA GCG GA? AAC AAA TTC 481
140 L L S E A K K L N E S Q A P K A D N K F 159

482 AAC AAA GAA CAA CAA AAT GCT TTC TAT GAA ATC TTA CAT TTA CCT AAC TTA AAC GAA GAA 541
170

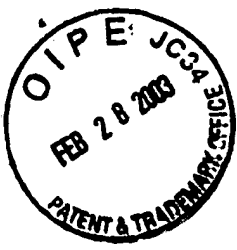


FIGURE 14A

1 ccatggctatacccaacctcggctcttggtcacaccaggaactctctggttaagctagctccactcccagaaacaaccggc a0
81 gccaaattgccggaattgctgacctgaagacggaacatcatcgctgggtccttgggcgattgcggcggaagatgggtcag 160
161 cttgggcttgaggacgagacccgaatcgagctctgttgaaaggttgctcattgggatttgatacggagattggctcgcga 240
241 gaggtttgagggaaaggacaaatgggtttggctctggagaaagagagtgcgg~tttagagagagaattgagaggtttaga 320
321 gagagatgcggcgcgatgacgggaggagagacgacgaggacctgcattatcaaagcagtgcgtggtgaaatttggaac 400
401 ttttaagaggcagatagatttattatttgatccattttcttcattgttctagaatgtcgcggaacaaattttaaaacta 4a0
481 aatcctaaatttttctaattttgttgccaatagtggatagtgggcccgtatagaaggaatc~attgaaggcccaaa~cca 560
561 tactgacgagcccaagggttcggttttgcttttatgtttcggttcgatgccaacgccacattctgagctaggcaaaaaac 640
641 aaacgtgtctttgaatagactcctctcgttaacacatgcagcggctgcattggtgacgccattaacacgtggcctacaatt 720
721 gcatgatgtctccattgacacgtgacttctcgtctcctttcttaatatatctaacaacactcctacctcttccaaaata 800
801 tatacacatctttttgatcaatctctcattcaaaatctcattctctctagtaaacaagaacaaaaa ATG GCG GAT a76
1 M A D 3
877 ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG TACCG ATG ATG GGC CGA 936
4 T A R G T H H D I I G R D Q Y P M M G R 23
937 GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC TCCAAG TCT AGG CAG ATT 996
24 D R D Q Y Q M S G R G S D Y S K S R Q I 43
997GCTAAAGCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC 1056
44 A K A A T A V T A G G S L L V L S S L T 63
1057 CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA 1116
64 L V G T V I A L T V A T P L L V I F S P 83
1117 ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA 1176
8 4 1 L V P A L I T V A L L I T G F L S S G 103
1177 GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatct 1241
104 G F G I A A I T V F S W I Y K 118
1242 tacttcataattttgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaattttttgggtcgaataacaaa 1321
1322 tgtaacaataagaaattgcaaattctagggaacatttgggttaactaaatacgaatttgacctagctagcttgaatgtgt 1401
1402 ctgtgtatatcatctatataggtaaaatgcttggtatgatacctattgattgtgaatag G TAC GCA ACG GGA 1473
119 Y A T G 122
1474 GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT 1533
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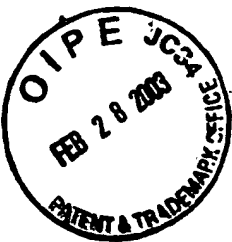


FIGURE 14B

1534 CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC 1593
143 Q D L K D R A Q Y Y G Q Q H T G G E H D 162

1594 CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT CTC GTT CCA CGA GGA TCC ATG GAT CAA 1653
163 R D R T R G G Q H T T L V P R G S M D Q 182

1654 CGCAATGGT TTT ATC CAA AGCCTT AAA GAT GAT CCA AGC CAA AGT GCT AAC GTT TTA GGT 1713
183 R N G F I Q S L K D D P S Q S A N V L G 202

1714 GAA GCT CAA AAA CTT AAT GAC TCT CAA GCT CCA AAA GCTGAT GCG CAA CAA AATAACTTC 1773
203 E A Q K L N D S Q A P K A D A Q Q N N F 222

1774 AAC AAA GAT CAA CAA AGC GCC TTC TAT GAA ATC TTG AAC ATG CCT AAC TTA AAC GAA GCG 1833
223 N K D Q Q S A F Y E I L N M P N L N E A 242

1834 CAA CGT AAC GGCTTCATTCAA AGT CTT AAA GAC GAC CCA AGC CAA AGC ACT AAC GTT TTA 1893
243 Q R N G F I Q S L K D D P S Q S T N V L 262

1894 GGT GAA GCT AAA AAA TTA AAC GAA TCT CAA GCA CCG AAA GCT GAT AAC AAT TTC AAC AAA 1953
263 G E A K K L N E S Q A P K A D N N F N K 282

1954 GAA CAA CAA AAT GCT TTC TAT GAA ATC TTGAATATG CCT AAC TTA AACGAA GAA CAA CGC 2013
283 E Q Q N A F Y E I L N M P N L N E E Q R 302

2014 AAT GGT TTC ATC CAA AGC TTA AAA GAT GAC CCA AGC CAA AGTGCT AAC CTA TTG TCA GAA 2073
303 N G F I Q S I K D D P S Q S A N L L S E 322

2074 GCT AAA AAGTTA AAT GAA TCTCAA GCA CCG AAA GCG GAT AAC AAA TTCAACAAA GAA CAA 2133
323 A K K L N E S Q A P K A D N K F N K E Q 342

2 13 4 CAA AAT GCT TTC TAT GAA ATC TTA CAT TTA CCT AAC TTA AACGAA GAA CAA CGC AAT GGT 2193
343 Q N A F Y E L L H L P N L N E E Q R N G 362

2 194 TTC ATC CAA AGC CTA AAA GAT GAC CCA AGC CAA AGC GCT AACCTT TTAGCA GAA XT AAA 2253
363 F I Q S L K D D P S Q S A N L L A E A K 332

2254 AAG CTA AATGAT GCT CAAGCA CCA AAA GCT GAC AAC AAA TTC AAC AAAGAA CAA CAA AAT 2313
383 K L N D A Q A P K A D N K F N K E Q Q N 402

2314 GCT TTC TAT GAA ATT TTA CAT TTA CCT AACTTA ACT GAA GAA CAA CGT AACGGCTTC ATC 2373
403A F YE IL H L P N L T E E Q R A G F I 422

2374 CAA AGC CTT AAA GAC GAT CCG GGG AAT TCC CGG GGA TCCGTCGAC CTG CAGATA ACA AA? 2433
423 Q S L K D D P G N S R G S V D L Q I T N 442

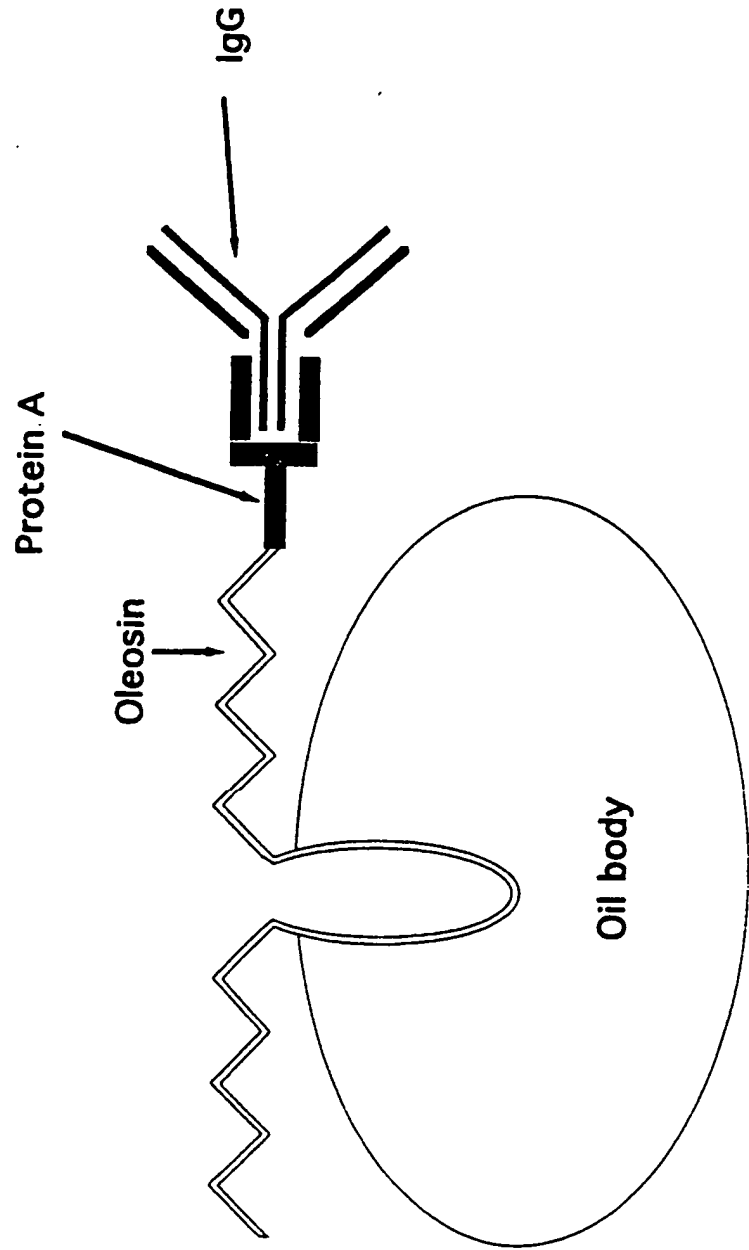
2434 TAG aagcttgcatgcctgcaggtcgatcggtt ttcaaacatttggcaataaagtttcttaagattgaatcctgttgccgggtc 2512
443 * 443

2513 ttgcgatgattatcatataatttctgttgtaattacgttaagcatgtaataattaacatgtaatgcatgacgttattttatg 2592

2593 agatgggtttttatgattagagtcccgcaattatacatttaatacgcgatagaaaacaaatatagcgcgcaactagga 2672

2673 taaattatcgcgcgggtgtcatctatgttactagat

FIGURE 15



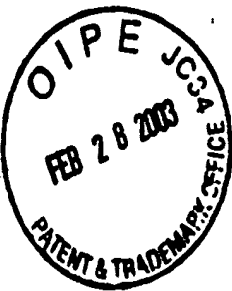


FIGURE 16

1 2 3 4 5 6 7 8 9

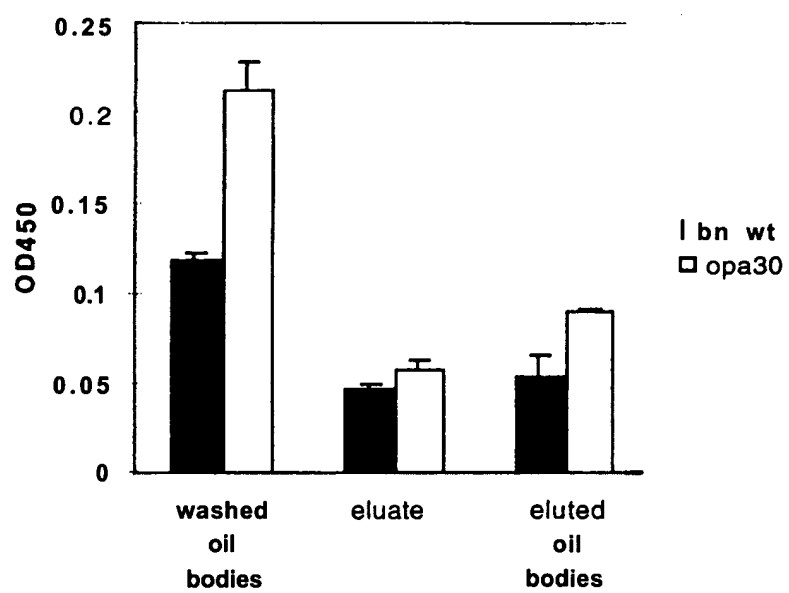
50 kDa →
(oleosin-protA)

30 kDa → —

(protA)



FIGURE 17



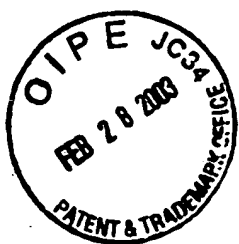


FIGURE 18A

1 ctgcaggaattcattgtactcccagatcattatagtgaaagtttttggtctctcgcgggtggtttttacctctattta 80
81 aaggggttttccacctaaaaattctggatcattctcactttacttgttacttttaatttctcataatctttgggtgaaat 160
161 taccagcttccgcacacgataccctacaaatttatatttgttaaacttttcaaaccgcataaaattttatgaagtc 240
241 ccgtctatctttaatgtagcttaacattttcatattgaaatatataatttacttaatttttagcgttggtagaaagcataa 320
321 agatttattcttattctttcatataaatgttttaataacataataaacaattctttaccttaagaaggatttcccat 400
401 tttataattttaaaaatatatttcaaatatttttcaaccacgtaaatctcataataataaagttgttcaaaagtaataa 480
481 aatttaactccataattttttattcgactgatcttaagcaacacccagtgacacaactagccattttttctttgaaat 560
561 aaaaaataccaattatcatctgtatttttttatacaatgaaaatttaccacaaacatttctgtggtatttctgaagcaa 640
641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720
721 ctcttaaagtaatttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800
801 ttagatataattaaaaattacttttttaattttaagtttaattgttgaatttgtgactattgatttatttctactat 880
881 gtttaaatgttttatagatagtttaaagtaaatataagtaagttagtagaggttagagtggtacccataaacataaac 960
961 tataacatttattggtggactaatttcatatatttcttattgttttaccttttcttggtatgtaagtcctgaactagaa 1040
1041 ttacagtggtgttgccatggcactctgtggtcttttggttcatgcatgggtcttgcgcaagaaaaagacaaagaacaaaga 1120
1121 aaaaagacaaaacagagagacaaaacgcaatcacacacacaaactcaaatagtcactggctgatcaagatcgccgcgtcc 1200
1201 atgtatgtctaaatgcatgcaaaagcaacacgtgcttaacatgcacttttaaatggctcaccatctcaaccacacacaa 1280
1281 acacattgctttttcttcatcatcaccac 1360
1361 aacacacgtcaacctgcatacgctgtcatcccatgcccacaaatcccatgcatgttcaaccacacacacacacacacacac 1440
1441 taccataaaatacctctaaatcactcacttcttctcatcatccatccatccagagtactactactctactactataatac 1520
1521 cccaacccaactcatattcaataactactctacc ATG AAC TTC CTT AAG TCT TTC CCT TTC TAC GCT 1586
1 M N F L K S F P F Y A 11
1587 TTC CTT TGT TTC GGT CAA TAC TTC GTT GCT GTT ACT CAC GCT ATG GCC GAG GTG AAG CTG 1646
12 F L C F G Q Y F V A V T H A M A E V K L 31
1647 CAG CAG TCT GGA GCT GAG CTG ATG AAG CCT GGG GCC TCA ATG AAG ATA TCC TGC AAG GCT 1706
32 Q Q S G A E L M K P G A S M K I S c K A 51
1707 AC? GGC TAC ACA TTC AGT AGC TAC TGG ATA GAG TGG GTA AAG CAG AGG CCT GGA CAT GGC 1766
52 T G Y T F S S Y W I E W v K Q R P G H G 71
1767 CTT GAG TGG ATT GGA GAG ATT TTA CCT GGC AGT GGT AGT ACT ACC TAC AAT GAG AAG TTC 1826
72 L E W I G E I L P G S G S T T Y N E K F 91
1827 AAG GGC AAG GCC ACA TTC ACT GCA GAT ACA TCC TCC AAC ACA GCC TAC ATG CAA CTC AGC 1886
92 K G K A T F T A D T S S N T A Y M Q L S 111
1887 AGC CTG ACA TCT GAG GAC TCT GCC GTC TAT TAC TGT GCA AGA TTG GAT GTT GAC TCC TGG 1946
112 s L T s E D S A V Y Y C A F L D V D s W 131
1947 GGC CAA GGC ACC ACT CTC ACC GTG TCG ACA GGT GGA GGC GGC TCT GGT GGC GGT GGC AGT 2006
132 G Q G T T L T V S T G G G G S G G G G S 151
2007 GGC GGC GGA GGT TCT GAC GTC GTG ATG ACC CAG TCT CCA TCC TCC CTG GCT ATG TCA GTG 2066
152 G G G G S D V V M T Q S P S S L A M S V 171
2067 GGA CAG CGG GTC ACT ATG CGC TGC AAG TCC AGT CAG AGC CTT TTA AAA AGT ACC AA? CAA 2126
172 G Q R V T M R C K S S Q S L L K S T N Q 191
2127 AAG AAC TAT TTG GCC TGG TAC CAG CAG AAA CCA GGA CAG TCT CCT AAA CTT CTG GTA TAC 2186
192 K N Y L A W Y Q Q K P G Q S P K L L V Y 211
2187 TTT GCA TCC ACT AGG GAA TCT GGG GTC CCT GAT CGC TTC ATA GGC AGT GGA TCT GGG ACA 2246
212 F A S T R E S G V P D R F I G S G S G T 231
2247 GAT TTC ACT CTT ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA GAT TAC TTC TGT CAG 2306
232 D F T I T I S S V Q A E D I A D Y F C Q 251
2307 CAA CAT TAT AAC ACT CCT CCC ACG TTC GGT GCT GGG ACC AAG CTG GAA ATC AAG CGC CTC 2366
252 Q H Y N T P P T F G A G T K L E I K R L 271

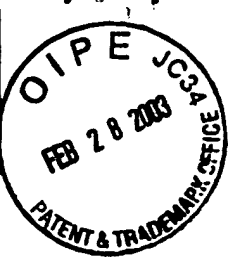


FIGURE 18B

2367 ATG GCT GAG ATC ACC CGC ATT CCT CTC TAC AAA GGT AAG TCT CTC CGT AAG GCG CTG AAG 2426
272 M A E IT R I P L Y K G K S L R K A L K 291
2427 GAA CAT GGA CTT CTA GAA GAC TTC TTG CAG AAA CAA CAG TAT GGC ATC AGC AGC AAG TAC 2486
292 E H G I L E D F L Q K Q Q Y G I S S K Y 311
2487 TCC GGC TTC GGT GAA GTT GCT AGC GTG CCA CTT ACC AAC TAC CTT GAT AGT CAA TAC TTT 2546
312 S G F G E / A S V P L T N Y L D S Q Y F 331
2547 GGG AAG ATC TAC CTC GGA ACC CCG CCT CAA GAG TTC ACC GTT CTC TTT GAT AC? GGT TCC 2606
332 G K I Y L G T P P Q E F T V L F D T G S 351
2607 TCT GAC TTC TGG GTT XC TCT ATC TAC TGC AAG AGC AAT GCC TGC AAG AAC CAC CAA AGA 2666
352 S D F w V P S I Y C K S N A C K N H Q R 371
2667 TTC GAT CCG AGA AAG TCG TCC ACC TTC CAG AAC TTA GGC AAA CCC TTG TCT ATA CAC TAC 2726
372 F D P R K S S T F Q N I G K P L S I H Y 391
2727 GGT ACA GGT AGC ATG CAA GGA ATC TTA GGC TAT GAT ACC GTC ACT GTC TCC AAC ATT GTG 2786
392 G T G S M Q G I L G Y D T V T V S N I V 411
2787 GAC ATT CAACAG ACA 'GTA GGA CTT AGC ACC CAA GAA CCA GGT GAT GTC TTC ACC TAT GCA 2846
412 D I Q Q T V G L S T Q E P G D V F T Y A 431
2847 GAA TTC GAT GGC ATC CTT GGT ATG GCA TAC CCA TCG CTC GCG TCA GAG TAC TCG ATA CCT 2906
432 E F D G I I G M A Y P S L A S E Y S I P 451
2907 GTG TTT GAC AAC ATG ATG AAC CGA CAC CTA GTA GCT CAA GAC TTG TTC TCG GTT TAC ATG 2966
452 V F D N M M N R H L V A Q D I F S V Y M 471
2967 GAC AGG AAT GGC CAG GAG AGC ATG CTC ACG CTT GGA GCT ATT GAT CCA TCC TAC TAC ACA 3026
472 D R N G Q E S I? I T I G A I D P S Y Y T 491
3027 GGA TCT CTT CAC TGG GTT CCA GTC ACT GTG CAG CAG TAC TGG CAA TTC ACT GTG GAC AGT 3086
492 G S L H W V P V T V Q Q Y W Q F T V D S 511
3087 GTC ACC ATC AGC GGT GTG GTT GTT GCA TGT GAA GGT GGA TGT CAA GCT ATC TTG GAT ACC 3146
512 V T I S G V V V A C E G G C Q A I L D T 531
3147 GGT ACG TCC AAG CTG GTC GGA CCT AGC AGC GAC ATT CTC AAC ATT CAG CAA GCT ATT GGA 3206
532 G T S K L V G P s S D I L N I Q Q A I G 551
3207 GCC ACA CAG AAC CAG TAC GGT GAG TTT GAC ATA GAT TGC TAC AAC CTT AGC TAC ATG CC? 3266
552 A T Q N Q Y G E F D I D c D N L S Y M P 571
7 ACA GTT GTC TTT GAG ATC AAC GGC AAG ATG TAC CCA CTG ACC 'CCC TCC GCC TAT ACC AGC 3326
572 T V V F E I N G K M Y P L T P S AY T S 591
3327 CAG GAT CAA GGG TTC TGC ACC AGT GGA TTC CAG AGT GAG AAC CAT TCC CAG AAA TGG ATC 3386
592 Q D Q G F C T S G F Q S E N H S Q K W I 611
3387 TTG GGA GAT GTG TTC AT? CGT GAG TAC TAC AGC GTC TTT GAC AGG GCC AAC AAC CTC GT? 3446
612 L G D V F I R E Y Y S V F D R A N N L V 631
3447 GGG CTA GCT AAA GCA ATC TGA agcttaataagtatgaactaaaaatgcatgtaggtgaagagctcatggagag 3519
632 G L A K .A I * 638
3520 catggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaggatgt 3599
3600 tatgatataattaacactctatctatgcaccttattgttctatgataaattccctcttattattataaatcatctgaatcg 3679
3680 tgacggcttatggaatgcttcaaatagtacaaaaaacaatgtgtactataagacttctaaacaattctaacttttagcat 3759
3760 tgtgaacgagacataagtgttaagaagacataacaattataatggaagaacttctctccatttatatattatattac 3839
3840 ccacttatgtattatattaggtgttaaggagacataacaattataaagagagaagttgtatccatttatattatattat 3919
3920 actacccatttatattataacttatccacttatttaatgtctttataagggttgatccatgatatttctaatttttag 3999
4000 ttgatatttatatgaaagggtactatttgaactctctactctgtataaagggttgatcatccttaagtggtgtctattt 4079



FIGURE 18C

4080 aattttattgcttcttacagataaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaa 4159
4160 taataaataacatataatatatgtatataaattttattataataataacatttatataaaaaagtaaatattgtcataaa 4239
4240 tctatacaatcgtttagccttgctggacgactctcaattatttaaagagagtaaacatatttgactttttggttattta 4319
4329 acaaattattttaaactatatgaaattttttttttttatcggcaaggaaataaaattaaattaggagggacaatggt 4399
4400 gtgtcccaatccttatacaaccaacttccacaggaagggtcaggtcggggacaacaaaaaacaggcaagggaattttt 4479
4480 aatttgggttgcttctgtttgtgcataatttatgcagtaaaacactacacataaccttttagcagtagagcaatgggtg 4559
4560 accgtgtgcttagcttctttttttttttttttatcagcaagaataaaataaaataaaatgagacacttcagggatgtt 4639
4640 tcaacctttatacaaaaacccccaaaaacaagtttcttagcacctaccaactaagggtacc 4698



FIGURE 19

